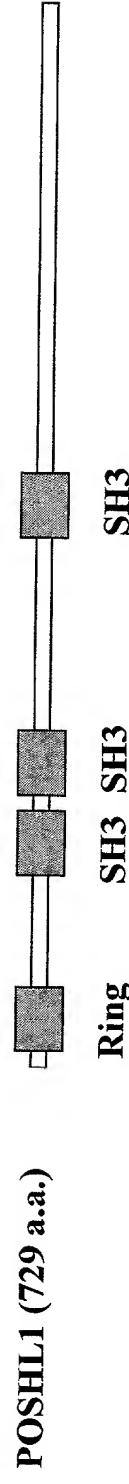


# Structure of the human POSHIL1 protein

**Fig. 1A**



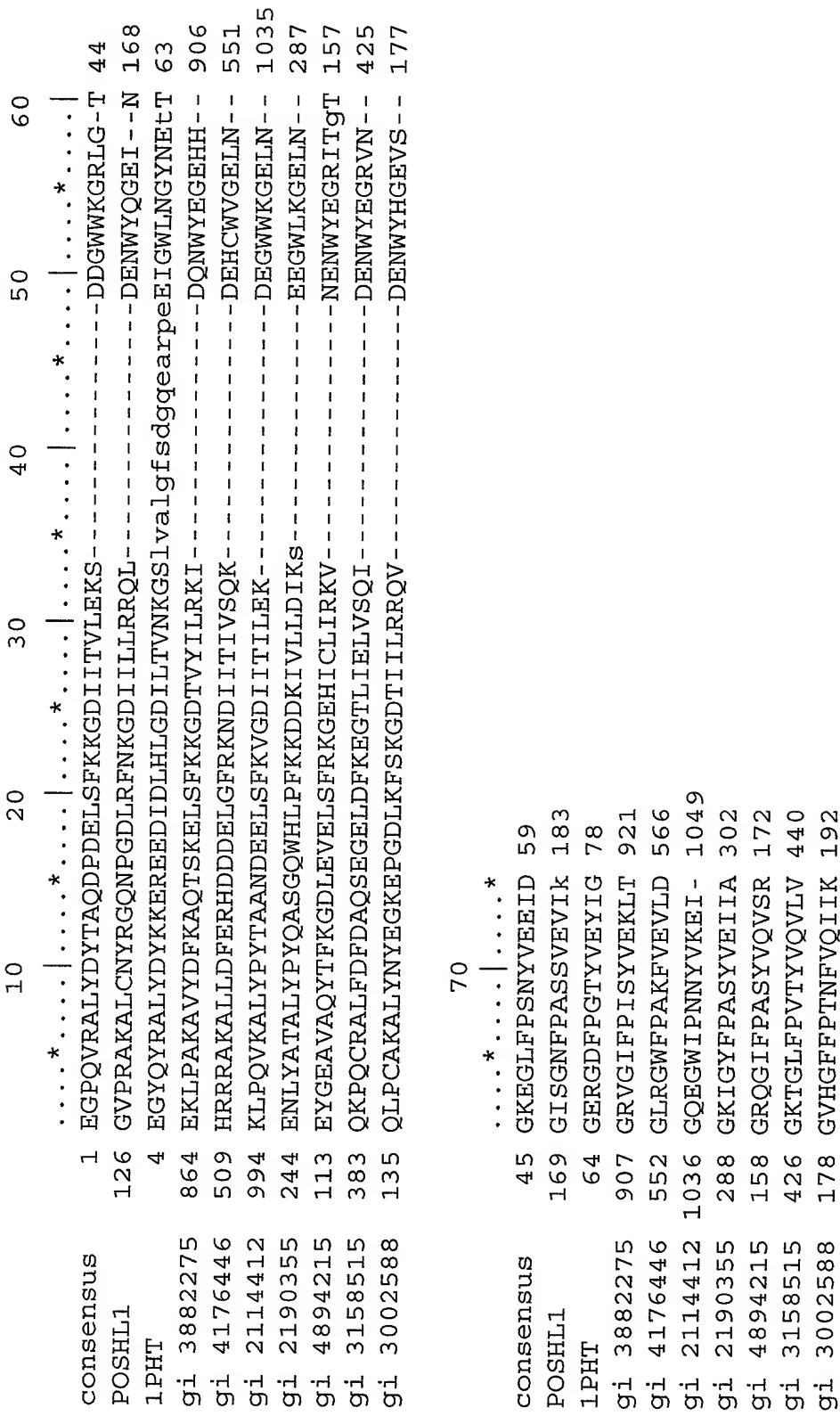
**Fig. 1B**

Ring Domain

		10	20	30	40
consensus	1	* . . .   . . . * . . .   . . . * . . .   . . . * . . .   . . . * . . .			
POSHIL1	12	CPICLLEEY - - - LKDPVVLP - CGHT - FCRSCIRKWLESSN - SNTCPIC	41		
1G25_A	6	CPRCKTTKyrnpSLKLMVNv - CGHT - LCESCVDLLFVRG - - AGNCPEC	52		
gi_2145348	18	CPVCLDL - - - FRVPITLM - CGHT - CCKHCLngiv - - KsdNARCPVC	49		
gi_2342720	91	CPVCLGLIPk - - - nVVIKVLPnCMHM - FDEECCIGKWLESHA - - - TCPVC	56		
gi_2738440	111	CVVCYEN - - - EICIKIQP - CNHFvVCKSCFNR - - - - LNTCPMC	132		
gi_3043558	71	CSICLER - - - YKNPKVLP - CLHT - FCERCLQNYIPAHS1tLSCPVC	145		
gi_3152606	28	CNICFEL - - - AQDPIVTL - CGHL - FCWPCLYRWLHHHshSQECPVC	111		
gi_3002588	12	CPVCLERL - - - DASAKVLP - CQHT - FCKRCLLGGIVGSRN - eLRCPEC	68		
gi_6226931	43	CPICLDR - - - YKQPKLLP - CQHT - FCYPCLESCADTLhmlKCPEC	52		
					83

# FIG. 1C

## SH3 Domain 1



# FIG. 1D

## SH3 Domain 2

11/3

		10	20	30	40	50	60
consensus	1	*** * . . .   * . . . * . . .   * . . . * . . .   * . . . * . . .   * . . . * . . .   * . . . * . . .					
POSHL1	188	PPPLCRALYNFD1rgkdkS	-A-----	QDPDELSFKKGDIITVLEKS	-	-	-DD 35
1PHT	4	EGYQQYRALYDYK-	-K-----	ENQDCLTFLKDDIITVVISRV	-	-	-DE 228
gi_3880771	408	VSPYARAVYDFQ-	-G-----	EREDIDILHLDILTVNKGS1valgfssdgqearpeEI	53	-	
gi_729368	153	EEMLVQALYDFV-	-P-----	EFENELSFSADEIIISLRRI	-	-DA 442	
gi_1346669	458	KGSQVEALFSYE-	-A-----	QESGELDFRRGDVITVTDRS	-	-DE 187	
gi_2961227	995	GPEQARALYDFA-	-A-----	TQPEDLEFQE GDP II ILVLSKV	-	-NE 492	
gi_2960022	3	QPLVQAEYSFM-	-G-----	ENPDELTFNNEGAVVTVINKS	-	-NP 1029	
gi_3002588	197	PPPQCKALYDFE-	-VkdkeADKDCLPFAKDDVLTVIRR	-	-DG 37		
gi_35999478	1160	TVGRCRALYDYG-	-A-----	QEADELTIREGDVIDVIQK	-	-DE 235	
					-SG 1193		
		70	80				
consensus	36	GWWKGRLG-TGKEGLFPSNYVEEID	59				
POSHL1	229	NWAEGKLG-D-KVGIFPILFVEPnl	251				
1PHT	54	GWLNGYNETTGERGDFPGTYVEYIG	78				
gi_3880771	443	EWLEGSIG-SARVGIFPSTS FVQIIIV	466				
gi_729368	188	NWWNGEIG--NRKGIFPATYVTPYH	210				
gi_1346669	493	EWLEGECK-GKVGIFPKVFVEDCA	515				
gi_2961227	1030	DWWEGELN--GQRGVFPASYVELIP	1052				
gi_2960022	38	GWWEGTLN--DKTGWFPSNYVNECK	60				
gi_3002588	236	NWAEGMLA--DKIGIFPISYVEFNS	258				
gi_35999478	1194	EWWEGLN--GKTGVFPANYVEDI-	1215				

FIG. 1E

SH3 Domain 3

	10	20	30	40	50
consensus	1	EGPQVRALLYDTAQDPDELISFKKGDIITVIEKS-----	*   * . . .   * . . .   * . . .   * . . .	-DDGWWKGR-LG-	4 3
POSHL1	381	SANMFVALHSYSAHGPDELLQKGEGVRVLGKC-----	- - - - -	- QDGWLRGVSLV-	4 2 4
1PHT	4	EGYQYRALYDYKKEREEDIDLHLGDLITVNKGSlvalgfssdggearpeIGWINGY-NET	- - - - -	- DDGWFVGT-SRR	7 0 7
gi	4322306	664 DLCSYQALYSYVPQNDDDELELRDGGIDVMEKC-----	- - - - -	- SDGWWWRGS-YN-	6 2
gi	127962	107 LNMPAYVKENYMAEREDELSLIKGTKVIVMEKC-----	- - - - -	- DAEWYRGK-CR-	1 6 8
gi	7619882	126 GAPHAVALHDFFPAEQADDLSLTSGEIVYLLIEKI-----	- - - - -	- DQAWILEGH-CD-	1 9 8
gi	3170194	156 VLYQVVAQHRYSAQGPEDLGFRQGDTVDVILCEV-----	- - - - -	- QDGWYKGT-SMh	4 9 6
gi	3002588	453 RPSVYVAIYPYTPRKEDDELELRKGEMFLVERC-----	- - - - -	- DDDWYEGV-LD-	4 2 2
gi	13324869	380 YLEKVRVLYDYDAAKEDELTLRENAIVVVIKKN-----	- - - - -	- SGDEGWWAGQ-VG-	8 9
gi	488296	42 ANPVWITALFDYEPESGQDELAIRKGDRVEVLSRDaa:i-----	- - - - -		
	70				
consensus	4 4	TGKEGLFEPNSNYVEEID	5 9		
POSHL1	4 2 5	TGRVGIFPNYYVIPIF	4 4 0		
1PHT	6 3	TGERGDFPDTYVEYIG	7 8		
gi	4322306	708 TRQFGTFPGNYVVKPLY	7 2 3		
gi	127962	150 -GQVGWFPSNYVTEEG	1 6 4		
gi	7619882	169 -NQTGVFPANYVKVIV	1 8 3		
gi	3170194	199 -GRIGIFPKCFVVPAG	2 1 3		
gi	3002588	4 9 7 TSKIGVFPGNYVAPVT	5 1 2		
gi	13324869	4 2 3 -GVTGLEPGNYVVPV-	4 3 6		
gi	488296	90 -GOVGVIEPSNYYVSRRGG	1 0 4		

## Structure of the POSHL1 gene (Chr. 5q32)

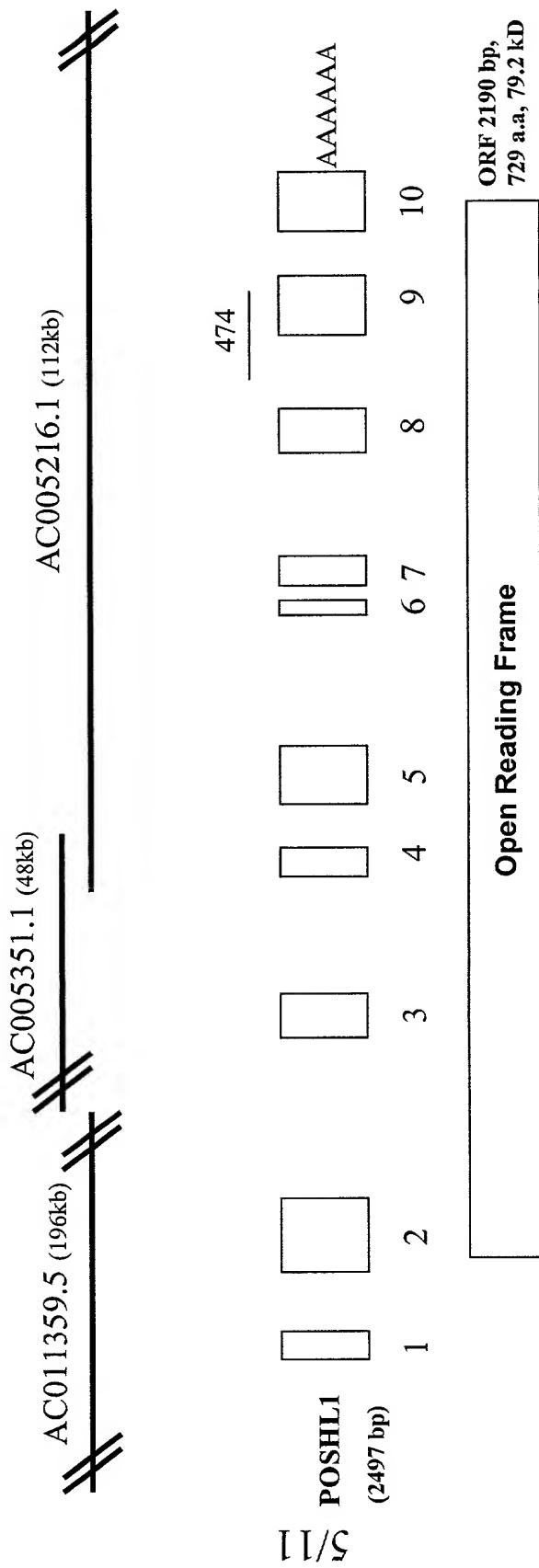


FIG. 2

**POSHL1**

**nt:** **SEQ ID NO:** 1  
**aa:** **SEQ ID NO:** 3

AAAGTTTCAAAGCGGTTGGCAGCAGCGCGCTTGGAGGAAAGGAAGCCGGT	52
TGGAGGGCGCAGCGCACCCCTGCTGCGCGAGGAGGGGGCTGAGCTGAACTC	104
AGCAGAAGTTACATGCACAAGGCAAAATTCTGACGTTCTCAAGAGACCAGC	156
TCTGCCCGTGGCTCAACTGACCTACCATGTGGACGCTGCTCCTCCAGGT	208
M D D L T L L	7
GGGAACTGGAGTTTGAAATAAA ATG GAT GAT TTG ACG TTA CTT	252
D L L E C P V C F E K L D	20
GAT CTT CTG GAG TGC CCT GTG TGC TTT GAG AAG CTC GAT	291
V T A K V L P C Q H T F C	33
GTC ACA GCC AAA GTC CTC CCT TGC CAG CAC ACC TTC TGC	330
K P C L Q R V F K A H K E	46
AAA CCA TGT CTA CAG AGG GTT TTC AAG GCC CAC AAA GAG	369
L R C P E C R T P V F S N	59
CTG CGG TGC CCC GAA TGC AGG ACG CCT GTG TTT TCC AAC	408
I E A L P A N L L V R L	72
ATT GAG GCG CTG CCG GCC AAC CTG CTG CTC GTG CGC CTT	447
L D G V R S G Q S S G R G	85
CTG GAT GGA GTG CGC TCA GGG CAG AGC TCC GGG AGA GGG	486
G S F R R P G T M T L Q D	98
GGC TCC TTC CGC AGG CCT GGC ACG ATG ACC TTG CAG GAT	525

**FIG. 3**

G	R	K	S	R	T	N	P	R	R	L	Q	A		111
GGC	AGG	AAA	AGC	AGG	ACC	AAC	CCC	AGA	CGT	CTG	CAG	GCC		564
S	P	F	R	L	V	P	N	V	R	I	H	M		124
AGT	CCT	TTC	CGG	CTA	GTG	CCT	AAT	GTC	AGA	ATC	CAC	ATG		603
D	G	V	P	R	A	K	A	L	C	N	Y	R		137
GAT	GGG	GTG	CCT	CGA	GCA	AAG	GCC	TTA	TGC	AAC	TAC	AGA		642
G	Q	N	P	G	D	L	R	F	N	K	G	D		150
GGG	CAG	AAT	CCC	GGT	GAC	CTA	AGG	TTT	AAT	AAG	GGA	GAT		681
I	I	L	L	R	R	Q	L	D	E	N	W	Y		163
ATC	ATC	CTT	CTC	CGG	AGA	CAG	CTT	GAT	GAG	AAT	TGG	TAC		720
Q	G	E	I	N	G	I	S	G	N	F	P	A		176
CAG	GGG	GAA	ATC	AAT	GGC	ATC	AGC	GGG	AAC	TTC	CCA	GCC		759
S	S	V	E	V	I	K	Q	L	P	Q	P	P		189
AGC	TCC	GTG	GAA	GTC	ATC	AAG	CAG	CTG	CCC	CAG	CCG	CCC		798
P	L	C	R	A	L	Y	N	F	D	L	R	G		202
CCG	CTC	TGC	AGG	GCC	CTC	TAC	AAC	TTC	GAC	CTA	CGA	GGC		837
K	D	K	S	E	N	Q	D	C	L	T	F	L		215
AAG	GAC	AAG	AGT	GAG	AAC	CAG	GAT	TGC	CTG	ACC	TTC	CTC		876
K	D	D	I	I	T	V	I	S	R	V	D	E		228
AAG	GAC	GAT	ATC	ACT	GTG	ATC	AGC	CGA	GTG	GAT	GAG			915
N	W	A	E	G	K	L	G	D	K	V	G	I		241
AAC	TGG	GCA	GAA	GGC	AAG	TTA	GGA	GAT	AAA	GTA	GGC	ATC		954
F	P	I	L	F	V	E	P	N	L	T	A	R		254
TTC	CCT	ATC	TTG	TTT	GTA	GAG	CCA	AAC	CTC	ACC	GCA	AGA		993
H	L	L	E	K	N	K	G	R	Q	S	S	C		267
CAC	CTT	TTA	GAG	AAG	AAC	AAA	GGT	CGC	CAG	TCA	TCC	TGC		1032
T	K	N	L	S	L	V	S	S	S	S	R	G		280
ACA	AAA	AAC	CTG	TCC	CTG	GTG	TCC	TCG	TCC	TCC	AGA	GGC		1071

FIG. 3

N	T	S	T	L	R	R	G	P	G	S	R	R		293
AAC	ACG	TCT	ACC	CTC	CGT	AGG	GGC	CCA	GGG	TCC	AGG	AGG		1110
K	V	P	G	Q	F	S	I	T	T	A	L	N		306
AAG	GTG	CCT	GGG	CAG	TTT	TCC	ATC	ACA	ACA	GCC	TTG	AAC		1149
T	L	N	R	M	V	H	S	P	S	G	R	H		319
ACT	CTC	AAC	CGG	ATG	GTC	CAT	TCT	CCT	TCA	GGG	CGC	CAT		1188
M	V	E	I	S	T	P	V	L	I	S	S	S		332
ATG	GTA	GAG	ATC	AGC	ACC	CCA	GTG	CTC	ATC	AGC	TCC	AGC		1227
N	P	S	V	I	T	Q	P	M	E	K	A	D		345
AAC	CCC	TCT	GTG	ATC	ACC	CAG	CCC	ATG	GAG	AAA	GCA	GAC		1266
V	P	S	S	C	V	G	Q	V	S	T	Y	H		358
GTT	CCT	TCC	AGC	TGT	GTG	GGA	CAG	GTC	AGC	ACT	TAT	CAC		1305
P	A	P	V	S	P	G	H	S	T	A	V	V		371
CCC	GCA	CCT	GTC	TCT	CCA	GGA	CAT	TCC	ACA	GCC	GTG	GTC		1344
S	L	P	G	S	Q	Q	H	L	S	A	N	M		384
AGT	CTG	CCT	GGC	TCC	CAG	CAA	CAC	CTC	TCA	GCG	AAC	ATG		1383
F	V	A	L	H	S	Y	S	A	H	G	P	D		397
TTT	GTA	GCC	CTG	CAC	TCC	TAC	TCA	GCC	CAT	GGA	CCC	GAT		1422
E	L	D	L	Q	K	G	E	G	V	R	V	L		410
GAG	CTG	GAC	CTG	CAA	AAG	GGA	GAA	GGC	GTC	AGG	GTC	CTG		1461
G	K	C	Q	D	G	W	L	R	G	V	S	L		423
GGG	AAG	TGC	CAG	GAC	GGC	TGG	CTC	AGG	GGC	GTC	TCC	TTG		1500
V	T	G	R	V	G	I	F	P	N	N	Y	V		436
GTC	ACC	GGG	CGA	GTC	GGC	ATC	TTC	CCA	AAC	AAT	TAC	GTC		1539
I	P	I	F	R	K	T	S	S	F	P	D	S		449
ATC	CCC	ATT	TTC	AGA	AAG	ACC	TCT	AGT	TTT	CCA	GAC	TCC		1578
R	S	P	G	L	Y	T	T	W	T	L	S	T		462
CGG	AGC	CCT	GGT	CTC	TAC	ACC	ACA	TGG	ACG	TTA	TCC	ACC		1617

FIG. 3

S	S	V	S	S	Q	G	S	I	S	E	G	D		475
TCC	TCT	GTG	TCC	TCC	CAA	GGC	AGC	ATT	TCA	GAA	GGT	GAT		1656
P	R	Q	S	R	P	F	K	S	V	F	V	P		488
CCA	CGG	CAA	AGC	CGT	CCC	TTC	AAA	TCC	GTC	TTT	GTG	CCC		1695
T	A	I	V	N	P	V	R	S	T	A	G	P		501
ACT	GCC	ATA	GTC	AAC	CCC	GTG	AGA	AGC	ACA	GCC	GGC	CCT		1734
G	T	L	G	Q	G	S	L	R	K	G	R	S		514
GGG	ACT	TTA	GGA	CAA	GGG	TCT	CTT	CGG	AAA	GGG	CGG	AGC		1773
S	M	R	K	N	G	S	L	Q	R	P	L	Q		527
AGC	ATG	AGA	AAG	AAT	GGA	TCC	CTG	CAG	AGA	CCC	CTC	CAG		1812
S	G	I	P	T	L	V	V	G	S	L	R	R		540
TCC	GGG	ATC	CCC	ACT	CTC	GTG	GTA	GGC	TCC	CTC	AGA	CGC		1851
S	P	T	M	V	L	R	P	Q	Q	F	Q	F		553
AGC	CCC	ACC	ATG	GTC	CTT	CGG	CCT	CAG	CAG	TTC	CAA	TTC		1890
Y	Q	P	Q	G	I	P	S	S	P	S	A	V		566
TAC	CAG	CCA	CAG	GGG	ATC	CCC	TCC	TCC	CCC	TCA	GCC	GTG		1929
V	V	E	M	G	S	K	P	A	L	T	G	E		579
GTG	GTG	GAG	ATG	GGG	TCC	AAG	CCT	GCC	CTC	ACG	GGG	GAG		1968
P	A	L	T	C	I	S	R	G	S	E	A	R		592
CCC	GCC	CTC	ACG	TGC	ATC	AGC	AGG	GGC	AGT	GAG	GCC	CGG		2007
T	H	S	A	A	S	S	L	I	M	E	D	K		605
ACC	CAC	TCC	GCG	GCC	AGC	TCC	CTC	ATT	ATG	GAA	GAC	AAA		2046
E	I	P	I	K	S	E	P	L	P	K	P	P		618
GAA	ATC	CCC	ATC	AAG	AGT	GAG	CCT	CTG	CCA	AAA	CCG	CCC		2085
A	S	A	P	P	S	I	L	V	K	P	E	N		631
GCA	TCT	GCC	CCA	CCA	TCC	ATC	CTG	GTG	AAA	CCA	GAA	AAC		2124
S	R	N	G	I	E	K	Q	V	K	T	V	R		644
TCA	AGA	AAT	GGC	ATC	GAA	AAG	CAA	GTC	AAA	ACC	GTG	AGA		2163

FIG. 3

F	Q	N	Y	S	P	P	P	T	K	H	Y	T		657
TTT	CAG	AAT	TAC	AGC	CCT	CCT	CCC	ACC	AAA	CAT	TAC	ACC		2202
S	H	P	T	S	G	K	P	E	Q	P	A	T		670
TCC	CAT	CCC	ACC	TCC	GGA	AAG	CCT	GAA	CAG	CCA	GCC	ACC		2241
L	K	A	S	Q	P	E	A	A	S	L	G	P		683
CTC	AAG	GCG	TCC	CAG	CCT	GAA	GCA	GCG	TCC	TTG	GGC	CCA		2280
E	M	T	V	L	F	A	H	R	S	G	C	H		696
GAG	ATG	ACC	GTC	CTA	TTT	GCC	CAC	CGA	AGT	GGC	TGC	CAC		2319
S	G	Q	Q	T	D	L	R	R	K	S	A	L		709
TCC	GGA	CAG	CAG	ACA	GAC	CTC	CGG	AGA	AAG	TCA	GCT	CTT		2358
A	K	A	T	T	L	V	S	T	A	S	G	T		722
GCC	AAG	GCC	ACA	ACC	CTG	GTG	TCC	ACT	GCC	TCA	GGC	ACG		2397
Q	T	V	F	P	S	K	*							730
CAG	ACC	GTG	TTT	CCC	AGC	AAA	TGA	ACCTACGGGTGACTTTCC						2440
TAGACCCCAAAGAGGTGAATTGCATTAAATACAGTCTGCCTCCACTAAAAAA														2492
AAAAAA														2497

# RT-PCR Analysis of POSHL1 Expression

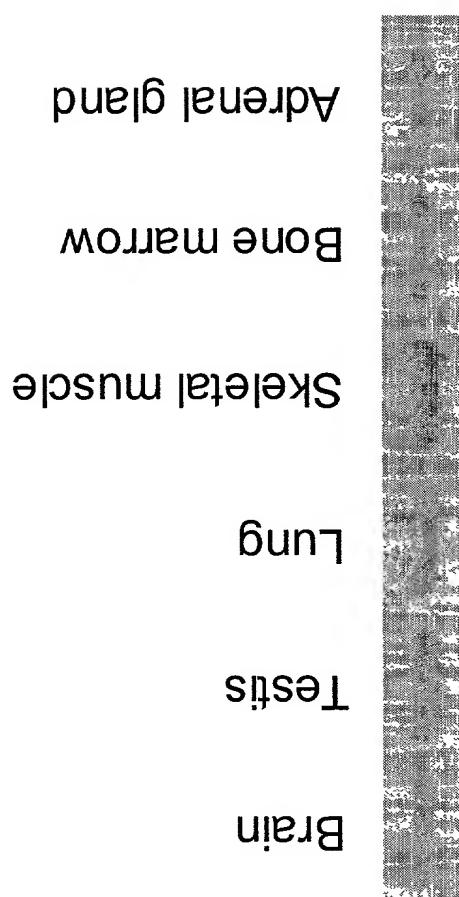


FIG. 4